

Human A4 Receptor

TM1	47-69
TM2	82-104
TM3	121-141
TM4	160-182
TM5	218-240
TM6	275-297
TM7	312 336

Figure 1

Amino Acid Homologies of A4 and Related Mammalian Receptors

Note: All sequences are human

Numbers below represent % similarity / % identity

A4	<i>Orexin1</i>	<i>Orexin2</i>	<i>Y1</i>	<i>Y2</i>	<i>Y4</i>	<i>Y5</i>	<i>Gastrin</i>	<i>CCKA</i>	<i>NK1</i>	<i>Mu</i>	
100	59/32	61/32	63/31	61/30	59/28	61/28	61/28	63/31	55/26	62/25	A4
	100	84/69	58/26	59/32	64/32	61/26	58/27	59/30	59/32	58/26	<i>Orexin1</i>
		100	60/27	60/31	63/32	59/26	61/29	58/29	56/31	58/28	<i>Orexin2</i>
			100	63/31	71/43	66/32	60/30	56/28	54/29	54/24	<i>Y1</i>
				100	62/33	63/32	56/27	56/29	59/30	57/24	<i>Y2</i>
					100	64/29	54/29	56/28	53/26	54/25	<i>Y4</i>
						100	58/28	55/26	57/24	61/26	<i>Y5</i>
							100	73/50	55/27	58/24	<i>Gastrin</i>
								100	57/30	55/26	<i>CCKA</i>
									100	60/26	<i>NK1</i>
										100	<i>Mu</i>

Legend:

<i>Code:</i>	<i>GenBank Assessment No.</i>	<i>Description</i>
Orexin 1	AF041243	Human Orexin receptor-1
Orexin2	AF041245	Human Orexin receptor-2
Y1	P25929	Human Neuropeptide receptor Type1
Y2	P49146	Human Neuropeptide receptor Type2
Y4	P50391	Human Neuropeptide receptor Type4
Y5	U56079	Human Neuropeptide receptor Type5
Gastrin	P32239	Human Gastrin/Cholecytokinin Type B receptor
CCKA	P32238	Human Cholecystokinin Type A receptor
NK1	P25103	Human Neurokinin-1 / Substance-P receptor
Mu	P35372	Human Mu-type opioid receptor

Data above was obtained using the GAP program from the WISCONSIN PACKAGE Version 9.0

Parameters used: Symbol comparison table: oldpep.cmp *

Gap Creation Penalty: 30

Gap ExtensionPenalty: 1

* This is the default scoring matrix used by versions of the Wisconsin Package prior to Version 9.0, based on the PAM250 table from M. Dayhoff¹.

1.) Schwartz, R. M. and Dayhoff, M. O. [1979]. Matrices for Detecting Distant Relationships. In *Atlas of Protein Sequence and Structure*, (M.O. Dayhoff, ed.), 5, Suppl. 3, (pp; 353-358), National Biomedical Research Foundation, Washington D.C., USA.

Figure 2

A4 vs. Human Y1 receptor

Percent Similarity: 63.032

Percent Identity: 30.585

Figure 3

Amino Acid Comparison

Human A4 Receptor vs. Human Orexin Receptor-2

Percent Similarity: 60.500

Percent Identity: 31.500

Gap Weight: 30

Length Weight: 1

Top sequence: Human Orexin receptor-2

Bottom Sequence: Human A4 receptor

1 MSGTKLEDSPPCRNWSSASELNETQEPFLNPTDYDDEEFLRYLWREYLHP 50
|...|.|..||:..:||:|:..:...:..:|||.
1 MNEKW..DTNSSENWHPIWNVNDTKHHLYSDINXTYVNY.....YLHQ 41
51 KEYEWVLIAGYIIVFVVALIGNVLVCVAWKNHHMRTVTNYFIVNLSLAD 100
..|.:|:..|:..:|..:..||..||.||:|..||:||||.||:||:..|
42 PQVAAIFIISXFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISD 91
101 VLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSLTLSCIAL 150
:||:| |:| ||: :|..:| ||:..:||: ..:|:||:..||:|| .||:
92 LLVGIFCMPITLLDNIAGWPFGNTMCKISGLVQGISVAASVFTLVIAV 141
151 DRWYAICHPLMFKSTAKRARNSIVIIWIVSCIIMIPQAIWME.....CST 195
||: .:.|:..| | | | | |:|||:..:|| | |:..: : : :
142 DRFQCVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYR 191
196 VFPGLANKTTLFTVCDERWGGEIYPKMYHICFLVTYMAPLCLMVLAYLQ 245
| : .|||. . | | | .: .|:| ..| .|:| |||:|:| :| :| :
192 VRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANITYLAPSLIVIMYGR 241
246 IFRKLWCRQIPGTSSVVQRWKPLQPVSQPRGPGQPTKSRSRMSAVAAEIKQ 295
| .|: ..| | ..| :| ..:|
242 IGIISLFRAAVPHTGEKNQEWHVV..... 265
296 IRARRKTARMLMVLLVFAICYLPISILNVLKRVFGMFAHTEDRETVYAW 345
| :|||. :||:| |:| :..| ||:..| :| . : : .. : ..|
266 SRKKQKIIKMLLIVALLFILSWLPLWTLMMMLSDYADLSPNELQIINIYI. 314
346 FTFSHWLVYANSAANPIIYNFLSGKFREEFKAFCSCCCLGVHHRQEDRLT 395
..|:|||. :||:| ..| |||||:| :..:|| :|:|| |.. : ..:
315 YPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFQ...LQLCQKRAKPME 361
396 RGRTSTESRKSLTT.....QISNFDN.....ISKLSEQVVLTSI 429
...|: ..| | | .|:| .| : ..| :| :|:
362 AYTLKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSAEKPQQELVMEEL 411
430 STLPAANGAGPLQNW* 445
... ..:.
412 KETTNSSSET*..... 421

Figure 4

A4 vs. Human CCK receptor

Percent Similarity: 63.514

Percent Identity: 31.081

1	..MNEKWDTNSSENWHPIWNVNNDTKHHLYSDINXTYVNYYLHQPV....	44
	: : . . : . . : . . : : : : :	
1	MDVVDSLLVNGS.....NITPPCELGLENEL..FCLDQPRPSKEW	39
45	.AAIFIISXFLIFFLCMMGNTVVCFIVMRNKHMHVTNLFILNLAISDLL	93
	: : : : : : . . : : : : : : : : :	
40	QPAVQILLYSLIFLSSLVLGNTLVITVLIRNKRMRVTNIFLSSLAVSDLM	89
94	VGIFCMPITLLDNIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDR	143
	: . : : . : : : . : : . . : :	
90	LCLFCMPFNLIPNLLKDFIFGSAVCKTTYFMGTSVSVSTFNLVAISLER	139
144	FQCVVYPFKPKL..TIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYR	191
	: . . . : : : . : . . : . : : : :	
140	YGAICKPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIYSNL.....	182
192	VRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGR	241
	. . . : : . : : : . : : : : : :	
183	VPFTKNNNQTA.NMCRFLLPNDVMQQSWHTFLLLILFLIPGIVMMVAYGL	231
242	IGISLFRA...AVPHTGRKNQEWHVVSRK.....	268
	: . : : :	
232	ISLELYQGIKFEASQKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLE	281
269KQKIIKMLLIVALLFILSWLPLWT	292
	: : : : : : : : : : :	
282	LRQLSTGSSSRANRIRNSAANLMAKKRVRIRMLIVIVVLFFLCWMPIFS	331
293	LMMLSDYADLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRR	342
	: . . : : . . : : : : : : . .	
332	ANAWRAYDTASAE..RRLSGTPISFILLSSYTSSCVNPIIYCFMNKRFRRL	379
343	GFQEAFQLQLCQKRAKPMEAYTLKAKSHVLINTSNQLVQESTFQNPHGET	392
	. : : . : : . : . : : : . : : :	
380	GFMATF.....PCCPNPGPPGARGEVGECEESEGTTGASLSRF	416
393	LLYRKSAEKPQQELVMEELKETTNSEEI*	421
	. . : . .	
417	SYSHMSASVPPQ.....	428

Figure 5

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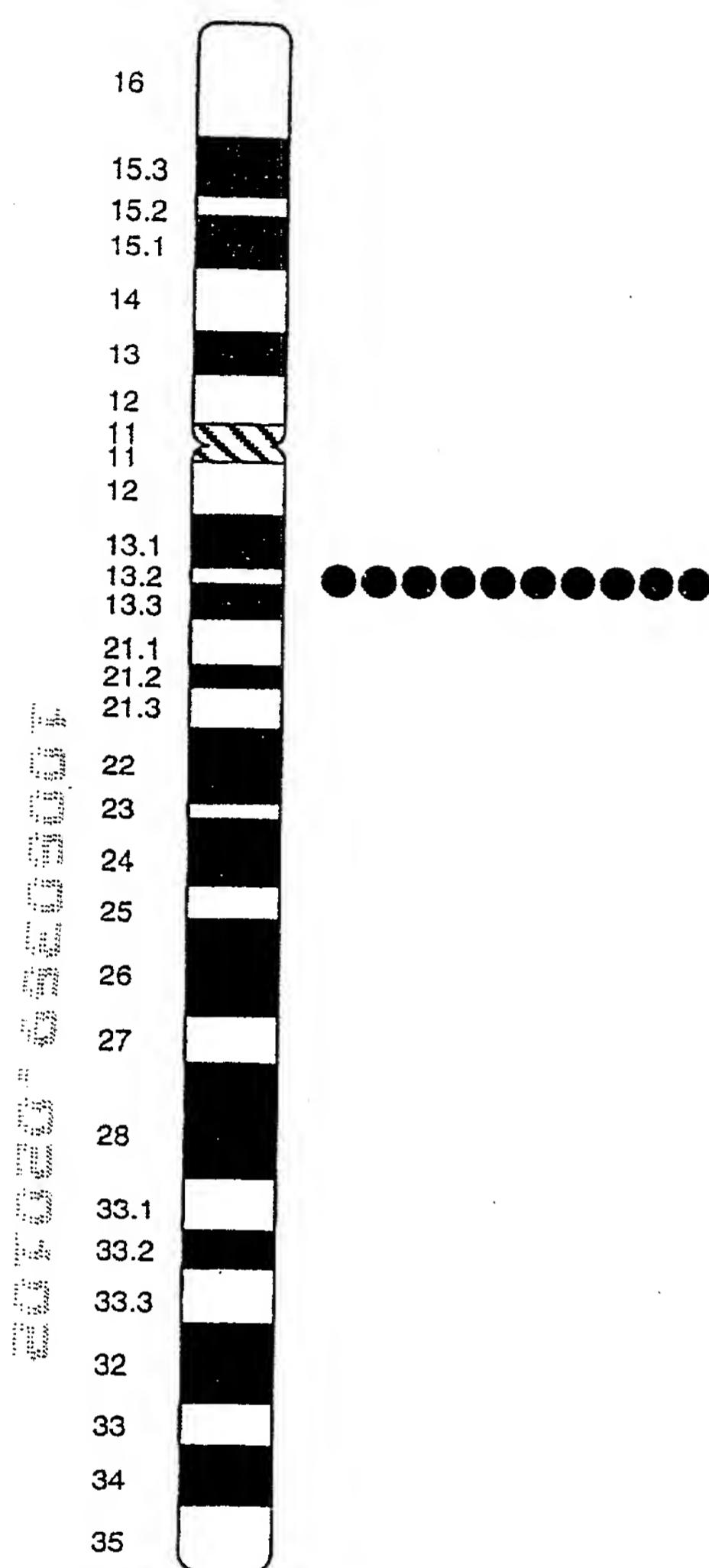


Figure 6